

STN SEARCH HISTORY

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 10:40:59 ON 28 AUG 2006

L1 1357 SEA HAC1 OR HACA OR ERN4 OR IRE1 OR IREA OR ERN1

L2 46 SEA (((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) HETEROLOGOUS)
(P) SECRET?)

L3 0 SEA L1 AND L2

L4 0 SEA ((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) HETEROLOGOUS) AND
L1

L5 219 SEA ((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) HETEROLOGOUS)

L6 22 SEA ((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) SECRET?) AND L1

L7 15 DUP REM L6 (7 DUPLICATES REMOVED)

L8 2 SEA L7 AND PY<2001
D L8,BIB,1-2
D L8,ABS,1~
D L8,ABS,2
D L8,BIB,2

L9 2634 SEA (UNFOLD? (A) PROTEIN (A) RESPONSE)

L10 657 SEA L9 AND L1

L11 123 SEA L10 AND (SECRET?)

L12 56 DUP REM L11 (67 DUPLICATES REMOVED)

L13 4 SEA L12 AND PY<2001
D L13,BIB,1-4

L14 4 SEA L13 AND (HAC1 OR HACA OR ERN4 OR IRE1 OR IREA OR ERN1)

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	595	Hac1 or HacA or Ern4 or IRe1 or IreA or Ern1	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:22
L2	12779	((protein or peptide or polypeptide) with heterologous) same secret\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:36
L3	85	L1 and L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:28
L4	115	unfold\$4 adj protein adj response	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:28
L5	21	L4 and L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:28
L6	10	L5 not L3	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:31
L7	47	L4 and (heterologous with (protein or peptide or polypeptide))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:31
L8	36	L7 not L3	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:31
L9	26	L8 not L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:34
L10	388	L1 and (yeast or fungi or fungus)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:34
L11	37	L10 and (unfold\$4 adj protein adj response)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:35

EAST Search History

L12	21	(unfold\$4 adj protein adj response) and (((protein or peptide or polypeptide) with heterologous) same secret\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:36
L13	10	L12 not L1	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:36
L14	0	L13 not L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/08/28 10:36

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-6_copy_53_116.rup.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:19 ; Search time 150.72 Seconds
(without alignments)
392.788 Million cell updates/sec

Title: US-10-663-450-6_COPY_53_116
Perfect score: 324
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	324	100.0	347	2	Q5AQN3_EMENI	Q5aqn3 aspergillus
2	324	100.0	350	2	Q8TFU8_EMENI	Q8tfu8 emericella
3	321	99.1	348	2	Q2U743_ASPOR	Q2u743 aspergillus
4	317	97.8	342	2	Q6W8X2_ASPNG	Q6w8x2 aspergillus

5	315	97.2	433	2	Q4WEY8_ASPEFU	Q4wey8 aspergillus
6	283	87.3	451	2	Q8TFF3_TRIRE	Q8tff3 trichoderma
7	282	87.0	430	2	Q7SHF0_NEUCR	Q7shf0 neurospora
8	265	81.8	556	2	Q2KH12_MAGGR	Q2kh12 magnaporthe
9	250	77.2	429	2	Q4HTT5_GIBZE	Q4htt5 gibberella
10	178.5	55.1	299	2	Q6CEV1_YARLI	Q6cev1 yarrowia li
11	174.5	53.9	273	2	Q6CKQ1_KLULA	Q6ckq1 kluyveromyc
12	171.5	52.9	230	1	HAC1 YEAST	P41546 saccharomyces
13	171	52.8	260	2	Q6BQC2_DEBHA	Q6bqc2 debaryomyces
14	166	51.2	228	2	Q75BQ5_ASHGO	Q75bq5 ashbya goss
15	166	51.2	357	2	Q5AA52_CANAL	Q5aa52 candida alb
16	144	44.4	329	2	Q6FLY3_CANGA	Q6fly3 candida glauca
17	117	36.1	336	2	Q5VR11_ORYSA	Q5vr11 oryza sativa
18	116	35.8	168	1	HY5_ARATH	Q24646 arabidopsis
19	109	33.6	69	2	Q58L60_BRACM	Q58160 brassica campestris
20	109	33.6	109	2	Q84XX8_BRARP	Q84xx8 brassica rapa
21	108	33.3	176	2	Q69XK6_ORYSA	Q69xk6 oryza sativa
22	105.5	32.6	141	2	Q677A7_HYAOR	Q677a7 hyacinthus
23	104.5	32.3	252	2	Q6NX18_XENTR	Q6nx18 xenopus tropicalis
24	103.5	31.9	158	1	HY5_LYCES	Q9sm50 lycopersicon esculentum
25	102.5	31.6	254	2	Q2TAU5_XENLA	Q2tau5 xenopus laevis
26	102.5	31.6	350	2	Q90ZR7_XENLA	Q90zr7 xenopus laevis
27	102.5	31.6	396	2	Q7ZYC2_XENLA	Q7zyc2 xenopus laevis
28	100	30.9	208	2	Q5DFK2_SCHJIA	Q5dfk2 schistosoma japonicum
29	100	30.9	321	2	Q8GRY7_LOTJA	Q8gry7 lotus japonicus
30	99	30.6	188	2	Q6ZHT8_ORYSA	Q6zht8 oryza sativa
31	98	30.2	120	2	Q682B6_ARATH	Q682b6 arabidopsis
32	98	30.2	149	1	HYH_ARATH	Q8w191 arabidopsis
33	97	29.9	322	2	Q39896_SOYBN	Q39896 glycine max
34	97	29.9	326	2	Q39895_SOYBN	Q39895 glycine max
35	96	29.6	261	2	Q3SZZ2_BOVIN	Q3szz2 bos taurus
36	95	29.3	703	2	Q4WC74_ASPEFU	Q4wc74 aspergillus
37	94.5	29.2	309	2	Q4H2M2_CIOIN	Q4h2m2 ciona intestinalis
38	94	29.0	322	2	Q04234_VICFA	Q04234 vicia faba
39	94	29.0	627	2	Q5BD44_EMENI	Q5bd44 aspergillus
40	92	28.4	263	2	Q8UVQ5_BRARE	Q8uvq5 brachydanio
41	92	28.4	263	2	Q90X27_BRARE	Q90x27 brachydanio
42	92	28.4	383	2	Q8QHJ5_BRARE	Q8qhj5 brachydanio
43	92	28.4	383	2	Q90XD3_BRARE	Q90xd3 brachydanio
44	92	28.4	646	2	Q6AU90_ORYSA	Q6au90 oryza sativa
45	91.5	28.2	260	2	Q6EZA7_OREMO	Q6eza7 oreochromis

ALIGNMENTS

RESULT 1

Q5AQN3_EMENI

ID Q5AQN3_EMENI PRELIMINARY; PRT; 347 AA.

AC Q5AQN3;

DT 26-APR-2005, integrated into UniProtKB/TrEMBL.

DT 26-APR-2005, sequence version 1.

DT 07-MAR-2006, entry version 8.

DE Hypothetical protein.

GN ORFNames=AN9397.2;

OS Aspergillus nidulans FGSC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI_TaxID=227321;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:33:51 ; Search time 18.56 Seconds
 (without alignments)
 331.782 Million cell updates/sec

Title: US-10-663-450-6_COPY_53_116

Perfect score: 324

Sequence: 1 KKPAKKRKSWGQELPVPKTN..... RAAAGTSRERKRLEMEKLES 64

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	171.5	52.9	238	2	S78571	transcription fact
2	116	35.8	168	2	T50922	bZIP protein HY5 {
3	97	29.9	322	2	T08592	TGACG-motif-bindin
4	97	29.9	326	2	T08591	TGACG-motif bindin
5	94	29.0	322	2	T12093	TGACG-motif bindin
6	90.5	27.9	176	2	B90087	hypothetical prote
7	90.5	27.9	506	2	D84609	hypothetical prote
8	87.5	27.0	260	1	A36299	transcription fact

9	87.5	27.0	266	2	JC7300	tax-responsive ele
10	87.5	27.0	267	2	JC4857	hepatocarcinogenes
11	86	26.5	600	2	T00759	hypothetical prote
12	83	25.6	688	2	T32750	hypothetical prote
13	82.5	25.5	515	2	A42140	box B-binding fact
14	82.5	25.5	516	2	A44494	cAMP-responsive el
15	81	25.0	360	2	T03373	probable G-box bin
16	81	25.0	468	2	S33222	transcription fact
17	81	25.0	483	2	S12741	transcription fact
18	79.5	24.5	486	2	JC4028	activating transcr
19	77.5	23.9	1851	2	T19964	hypothetical prote
20	77	23.8	433	2	JC1230	DNA-binding protei
21	76.5	23.6	242	2	S05453	transcription fact
22	76	23.5	207	2	T40067	hypothetical prote
23	76	23.5	264	2	T24253	hypothetical prote
24	76	23.5	331	2	S33223	transcription fact
25	76	23.5	445	2	T50972	probable zuotin [i
26	75.5	23.3	246	2	T12585	Dc3 promoter-bindi
27	75.5	23.3	313	2	A34785	DNA-binding protei
28	75.5	23.3	349	2	A41349	histone-specific t
29	75.5	23.3	349	2	S77570	transcription fact
30	75.5	23.3	351	2	A45377	transcription fact
31	75.5	23.3	358	2	C42026	cyclic AMP respons
32	75.5	23.3	389	1	A39429	cAMP response elem
33	75.5	23.3	448	2	A42026	cAMP response elem
34	75.5	23.3	456	2	B42026	cyclic AMP respons
35	75.5	23.3	505	1	S05380	transcription fact
36	75.5	23.3	849	1	S64732	scaffold attachmen
37	75.5	23.3	1359	2	T34036	hypothetical prote
38	75	23.1	381	2	S26812	transcription fact
39	75	23.1	1549	1	A40691	trichohyalin - she
40	74.5	23.0	313	2	S66312	G-box binding fact
41	74.5	23.0	315	2	S20883	G-box-binding fact
42	74.5	23.0	315	2	G85433	G-box-binding fact
43	74.5	23.0	338	1	TVMSFB	transforming prote
44	74.5	23.0	338	2	I53043	transforming prote
45	74.5	23.0	452	2	H96710	hypothetical prote

ALIGNMENTS

RESULT 1

S78571

transcription factor HAC1 - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein YFL031w

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: S78571; S56223; S53578

R;Murakami, Y.

submitted to the Protein Sequence Database, January 1998

A;Reference number: S78570

A;Accession: S78571

A;Molecule type: DNA

A;Residues: 1-238

A;Cross-references: UNIPROT:P41546; UNIPARC:UPI0000157F61; EMBL:D50617; MIPS:YFL031w

A;Note: this is a revision to the sequence from reference S56186

R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasa submitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces*

A;Reference number: S56186

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:15 ; Search time 133.12 Seconds
(without alignments)
219.816 Million cell updates/sec

Title: US-10-663-450-6_COPY_53_116
Perfect score: 324
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	324	100.0	349	8	ADS12805	Ads12805 Aspergill
2	324	100.0	349	8	ADS12803	Ads12803 Aspergill
3	324	100.0	349	8	ADS12863	Ads12863 Aspergill
4	324	100.0	350	4	AAB82976	Aab82976 Aspergill
5	324	100.0	350	5	AAE15372	Aae15372 Aspergill
6	320	98.8	64	5	AAE15374	Aae15374 Aspergill
7	317	97.8	342	4	AAB82977	Aab82977 Aspergill
8	317	97.8	342	5	AAE15381	Aae15381 Aspergill
9	317	97.8	342	8	ADS12818	Ads12818 Aspergill
10	317	97.8	386	5	AAE15379	Aae15379 Aspergill
11	317	97.8	386	8	ADS12815	Ads12815 Aspergill
12	283	87.3	64	5	AAE15373	Aae15373 Trichoder
13	283	87.3	450	4	AAB82975	Aab82975 Trichoder
14	283	87.3	451	5	AAE15371	Aae15371 Trichoder
15	283	87.3	451	8	ADS12801	Ads12801 Trichoder
16	283	87.3	451	8	ADS12804	Ads12804 Trichoder
17	277	85.5	409	7	ABO43144	Abo43144 A. thalia
18	277	85.5	409	7	ADB31925	Adb31925 Plant (A.
19	277	85.5	409	8	ADO02271	Ado02271 Thalecres
20	171.5	52.9	84	5	ABP02534	Abp02534 Human ORF
21	171.5	52.9	200	8	ADS43437	Ads43437 Bacterial
22	171.5	52.9	230	2	AAW53806	Aaw53806 Transcrip
23	171.5	52.9	230	8	ADT87049	Adt87049 Yeast Str
24	171.5	52.9	238	2	AAW53807	Aaw53807 Transcrip
25	170	52.5	68	5	AAE15382	Aae15382 Yeast HAC
26	170	52.5	68	8	ADS12859	Ads12859 Saccharom
27	116	35.8	168	5	AAU93013	Aau93013 Arabidops
28	116	35.8	168	7	ADD30174	Add30174 Plant yie
29	116	35.8	168	8	ADI43893	Adi43893 Plant tra
30	116	35.8	211	3	AAG08861	Aag08861 Arabidops
31	111.5	34.4	192	4	AAB82614	Aab82614 Maize roo
32	111.5	34.4	192	4	AAB82615	Aab82615 Maize roo
33	111.5	34.4	192	4	AAB82616	Aab82616 Maize roo
34	111.5	34.4	192	4	AAG66525	Aag66525 Maize roo
35	111.5	34.4	192	4	AAG66526	Aag66526 Maize roo
36	109.5	33.8	185	9	ADW17162	Adw17162 Eucalyptu
37	106.5	32.9	170	8	ADM48147	Adm48147 Polypepti
38	106	32.7	163	9	ADW17580	Adw17580 Pinus rad
39	100	30.9	143	3	AAB33151	Aab33151 Pinus rad
40	98	30.2	120	3	AAG27808	Aag27808 Arabidops
41	98	30.2	135	3	AAG07181	Aag07181 Arabidops
42	98	30.2	149	3	AAG07180	Aag07180 Arabidops
43	98	30.2	149	3	AAG27807	Aag27807 Arabidops
44	98	30.2	188	3	AAG27806	Aag27806 Arabidops
45	93.5	28.9	672	8	ADX95805	Adx95805 Plant ful

ALIGNMENTS

RESULT 1

ADS12805

ID ADS12805 standard; protein; 349 AA.

XX

AC ADS12805;

XX

DT 16-DEC-2004 (first entry)

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450- 5_copy_84_147.rup.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:19 ; Search time 150.72 Seconds
(without alignments)
392.788 Million cell updates/sec

Title: US-10-663-450-5_COPY_84_147

Perfect score: 323

Sequence: 1 EKKPVKKRKSGQVLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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%

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4	292	90.4	342	2	Q6W8X2_ASPPNG	Q6w8x2 aspergillus

5	288	89.2	347	2	Q5AQN3_EMENI	Q5aqn3 aspergillus
6	288	89.2	348	2	Q2U743_ASPOR	Q2u743 aspergillus
7	288	89.2	350	2	Q8TFU8_EMENI	Q8tfu8 emericella
8	286	88.5	429	2	Q4HTT5_GIBZE	Q4htt5 gibberella
9	285	88.2	433	2	Q4WEY8_ASPOFU	Q4wey8 aspergillus
10	178	55.1	260	2	Q6BQC2_DEBHA	Q6bqc2 debaryomyce
11	178	55.1	273	2	Q6CKQ1_KLULA	Q6ckq1 kluyveromyc
12	175.5	54.3	299	2	Q6CEV1_YARLI	Q6cev1 yarrowia li
13	175	54.2	230	1	HAC1 YEAST	P41546 saccharomyc
14	174	53.9	357	2	Q5AA52_CANAL	Q5aa52 candida alb
15	168	52.0	228	2	Q75BQ5_ASHGO	Q75bq5 ashbya goss
16	148	45.8	329	2	Q6FLY3_CANGA	Q6fly3 candida gla
17	107	33.1	336	2	Q5VR11_ORYSA	Q5vr11 oryza sativ
18	106	32.8	168	1	HY5_ARATH	O24646 arabidopsis
19	102	31.6	69	2	Q58L60_BRACM	Q58l60 brassica ca
20	102	31.6	109	2	Q84XX8_BRARP	Q84xx8 brassica ra
21	101	31.3	158	1	HY5_LYCES	Q9sm50 lycopersico
22	100.5	31.1	141	2	Q677A7_HYAOR	Q677a7 hyacinthus
23	98	30.3	176	2	Q69XK6_ORYSA	Q69xk6 oryza sativ
24	96	29.7	252	2	Q6NX18_XENTR	Q6nx18 xenopus tro
25	94	29.1	188	2	Q6ZHT8_ORYSA	Q6zht8 oryza sativ
26	94	29.1	321	2	Q8GRY7_LOTJA	Q8gry7 lotus japon
27	94	29.1	646	2	Q6AU90_ORYSA	Q6au90 oryza sativ
28	94	29.1	686	2	Q61D33_CAEBR	Q61d33 caenorhabdi
29	93	28.8	120	2	Q682B6_ARATH	Q682b6 arabidopsis
30	93	28.8	149	1	HYH_ARATH	Q8w191 arabidopsis
31	92	28.5	254	2	Q2TAU5_XENLA	Q2tau5 xenopus lae
32	92	28.5	350	2	Q90ZR7_XENLA	Q90zr7 xenopus lae
33	92	28.5	396	2	Q7ZYC2_XENLA	Q7zyc2 xenopus lae
34	92	28.5	460	2	Q93XA0_PHAU	Q93xa0 phaseolus v
35	91	28.2	322	2	Q39896_SOYBN	Q39896 glycine max
36	91	28.2	326	2	Q39895_SOYBN	Q39895 glycine max
37	90.5	28.0	690	2	Q44743_CAEEL	O44743 caenorhabdi
38	90	27.9	379	2	Q3UNH6_MOUSE	Q3unh6 m bone marr
39	90	27.9	404	1	CREB3_MOUSE	Q61817 mus musculu
40	89	27.6	371	2	Q5TCV1_HUMAN	Q5tcv1 homo sapien
41	89	27.6	371	2	Q5R5Z9_PONPY	Q5r5z9 pongo pygma
42	89	27.6	395	1	CREB3_HUMAN	O43889 homo sapien
43	88.5	27.4	208	2	Q5DFK2_SCHJA	Q5dfk2 schistosoma
44	88.5	27.4	437	2	Q569T3_XENLA	Q569t3 xenopus lae
45	88	27.2	322	2	Q04234_VICFA	O04234 vicia faba

ALIGNMENTS

RESULT 1

Q8TFF3_TRIRE
 ID Q8TFF3_TRIRE PRELIMINARY; PRT; 451 AA.
 AC Q8TFF3;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2002, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Transcription factor.
 GN Name=hac1;
 OS Trichoderma reesei (Hypocreja jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocreja.
 OX NCBI_TaxID=51453;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-6_copy_53_116.rapbn.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:44:20 ; Search time 8.64 Seconds
(without alignments)
169.226 Million cell updates/sec

Title: US-10-663-450-6_COPY_53_116
Perfect score: 324
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%
	Query

No.	Score	Match Length	DB	ID	Description
1	251	77.5	425	6 US-10-449-902-40262	Sequence 40262, A
2	106	32.7	134	6 US-10-953-349-13422	Sequence 13422, A
3	106	32.7	134	6 US-10-953-349-22329	Sequence 22329, A
4	106	32.7	191	6 US-10-953-349-13421	Sequence 13421, A
5	106	32.7	191	6 US-10-953-349-22328	Sequence 22328, A
6	97	29.9	199	6 US-10-953-349-12209	Sequence 12209, A
7	97	29.9	201	6 US-10-953-349-20562	Sequence 20562, A
8	97	29.9	318	6 US-10-953-349-12208	Sequence 12208, A
9	97	29.9	320	6 US-10-953-349-20561	Sequence 20561, A
10	97	29.9	324	6 US-10-953-349-12207	Sequence 12207, A
11	97	29.9	326	6 US-10-953-349-20560	Sequence 20560, A
12	92	28.4	646	6 US-10-449-902-51369	Sequence 51369, A
13	80.5	24.8	293	6 US-10-953-349-23767	Sequence 23767, A
14	80.5	24.8	318	6 US-10-953-349-23766	Sequence 23766, A
15	80.5	24.8	323	6 US-10-953-349-23765	Sequence 23765, A
16	79.5	24.5	675	6 US-10-449-902-42244	Sequence 42244, A
17	78	24.1	296	6 US-10-953-349-24027	Sequence 24027, A
18	78	24.1	362	6 US-10-953-349-24026	Sequence 24026, A
19	78	24.1	382	6 US-10-953-349-24025	Sequence 24025, A
20	78	24.1	611	7 US-11-321-421-81	Sequence 81, Appl
21	77	23.8	332	6 US-10-953-349-23520	Sequence 23520, A
22	75.5	23.3	335	6 US-10-449-902-34705	Sequence 34705, A
23	75.5	23.3	467	6 US-10-449-902-38097	Sequence 38097, A
24	75.5	23.3	675	7 US-11-293-697-3326	Sequence 3326, Ap
25	75	23.1	142	6 US-10-449-902-31867	Sequence 31867, A
26	75	23.1	147	6 US-10-953-349-36806	Sequence 36806, A
27	75	23.1	165	6 US-10-953-349-36805	Sequence 36805, A
28	75	23.1	186	6 US-10-953-349-36804	Sequence 36804, A
29	75	23.1	457	6 US-10-449-902-53115	Sequence 53115, A
30	75	23.1	523	6 US-10-449-902-56056	Sequence 56056, A
31	75	23.1	650	6 US-10-449-902-44708	Sequence 44708, A
32	74	22.8	301	6 US-10-449-902-43842	Sequence 43842, A
33	73	22.5	380	6 US-10-449-902-43338	Sequence 43338, A
34	73	22.5	467	7 US-11-293-697-3606	Sequence 3606, Ap
35	72.5	22.4	237	6 US-10-953-349-34004	Sequence 34004, A
36	72.5	22.4	621	6 US-10-449-902-45462	Sequence 45462, A
37	72.5	22.4	621	6 US-10-449-902-52809	Sequence 52809, A
38	72	22.2	188	6 US-10-449-902-39656	Sequence 39656, A
39	72	22.2	357	6 US-10-449-902-50208	Sequence 50208, A
40	72	22.2	393	6 US-10-449-902-41469	Sequence 41469, A
41	71	21.9	215	6 US-10-449-902-45271	Sequence 45271, A
42	71	21.9	223	6 US-10-449-902-31526	Sequence 31526, A
43	71	21.9	279	6 US-10-953-349-25745	Sequence 25745, A
44	70.5	21.8	281	6 US-10-971-483-2	Sequence 2, Appli
45	70	21.6	167	6 US-10-449-902-40094	Sequence 40094, A

ALIGNMENTS

RESULT 1

US-10-449-902-40262

; Sequence 40262, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:42:39 ; Search time 100.8 Seconds
(without alignments)
294.105 Million cell updates/sec

Title: US-10-663-450-6_COPY_53_116
Perfect score: 324
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	324	100.0	349	3	US-09-816-277-4	Sequence 4, Appli
2	324	100.0	349	3	US-09-816-277-6	Sequence 6, Appli
3	324	100.0	349	4	US-10-663-450-4	Sequence 4, Appli
4	324	100.0	349	4	US-10-663-450-6	Sequence 6, Appli
5	317	97.8	342	3	US-09-816-277-19	Sequence 19, Appli
6	317	97.8	342	4	US-10-663-450-19	Sequence 19, Appli
7	317	97.8	386	3	US-09-816-277-16	Sequence 16, Appli
8	317	97.8	386	4	US-10-663-450-16	Sequence 16, Appli
9	283	87.3	451	3	US-09-816-277-2	Sequence 2, Appli
10	283	87.3	451	3	US-09-816-277-5	Sequence 5, Appli
11	283	87.3	451	4	US-10-663-450-2	Sequence 2, Appli
12	283	87.3	451	4	US-10-663-450-5	Sequence 5, Appli
13	277	85.5	409	3	US-09-533-029-104	Sequence 104, App
14	277	85.5	409	4	US-10-295-403-158	Sequence 158, App
15	277	85.5	409	4	US-10-412-699B-684	Sequence 684, App
16	250	77.2	174	4	US-10-767-701-61238	Sequence 61238, A
17	171.5	52.9	200	4	US-10-369-493-21867	Sequence 21867, A
18	170	52.5	68	3	US-09-816-277-60	Sequence 60, Appli
19	170	52.5	68	4	US-10-663-450-60	Sequence 60, Appli
20	117	36.1	203	4	US-10-437-963-151695	Sequence 151695,
21	117	36.1	203	5	US-10-732-923-13694	Sequence 13694, A
22	117	36.1	203	5	US-10-732-923-13695	Sequence 13695, A
23	116	35.8	168	3	US-09-934-455-102	Sequence 102, App
24	116	35.8	168	4	US-10-225-066A-206	Sequence 206, App
25	116	35.8	168	4	US-10-374-780A-2356	Sequence 2356, Ap
26	116	35.8	168	5	US-10-732-923-13692	Sequence 13692, A
27	116	35.8	168	5	US-10-225-066A-206	Sequence 206, App
28	111.5	34.4	192	3	US-09-772-656-2	Sequence 2, Appli
29	111.5	34.4	192	3	US-09-772-656-6	Sequence 6, Appli
30	111.5	34.4	192	3	US-09-772-656-10	Sequence 10, Appli
31	111.5	34.4	192	4	US-10-396-199A-2	Sequence 2, Appli
32	111.5	34.4	192	4	US-10-396-199A-6	Sequence 6, Appli
33	111.5	34.4	192	4	US-10-396-199A-10	Sequence 10, Appli
34	111	34.3	147	4	US-10-425-115-187302	Sequence 187302,
35	109	33.6	109	5	US-10-732-923-13697	Sequence 13697, A
36	109	33.6	196	4	US-10-425-115-197786	Sequence 197786,
37	108	33.3	176	4	US-10-437-963-164243	Sequence 164243,
38	106.5	32.9	170	4	US-10-310-154-565	Sequence 565, App
39	104.5	32.3	191	4	US-10-424-599-177263	Sequence 177263,
40	104	32.1	181	5	US-10-732-923-450	Sequence 450, App
41	101	31.2	217	4	US-10-425-115-197783	Sequence 197783,
42	100	30.9	143	5	US-10-856-499-1930	Sequence 1930, Ap
43	99	30.6	114	4	US-10-425-115-246430	Sequence 246430,
44	99	30.6	360	4	US-10-437-963-165206	Sequence 165206,
45	98	30.2	149	5	US-10-732-923-13693	Sequence 13693, A

ALIGNMENTS

RESULT 1

US-09-816-277-4

```

; Sequence 4, Application US/09816277
; Publication No. US20010034045A1
; GENERAL INFORMATION:
; APPLICANT: Penttila, Merja E.
; APPLICANT: Ward, Michael
; APPLICANT: Wang, Huaming
; APPLICANT: Valkonen, Mari J.
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Increased Production of Secreted

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SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450

6_copy_53_116.rai.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:41:45 ; Search time 29.44 Seconds
(without alignments)
190.284 Million cell updates/sec

Title: US-10-663-450-6_COPY_53_116
Perfect score: 324
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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
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1	277	85.5	409	2	US-09-533-029-104	Sequence 104, App
2	166	51.2	248	2	US-09-248-796A-18840	Sequence 18840, A
3	100	30.9	143	2	US-09-640-211A-1930	Sequence 1930, Ap
4	91.5	28.2	102	2	US-09-640-211A-1046	Sequence 1046, Ap
5	91	28.1	264	2	US-09-949-016-10789	Sequence 10789, A
6	87.5	27.0	260	2	US-09-538-092-950	Sequence 950, App
7	86	26.5	667	2	US-09-248-796A-14492	Sequence 14492, A
8	84.5	26.1	521	1	US-08-721-684C-2	Sequence 2, Appli
9	84.5	26.1	521	1	US-09-005-970-2	Sequence 2, Appli
10	84.5	26.1	521	2	US-09-407-715-2	Sequence 2, Appli
11	83	25.6	23	2	US-09-831-642-72	Sequence 72, Appli
12	80	24.7	212	2	US-09-489-039A-13074	Sequence 13074, A
13	79	24.4	63	2	US-09-107-433-3674	Sequence 3674, Ap
14	78	24.1	611	2	US-09-216-393B-81	Sequence 81, Appli
15	77.5	23.9	1601	2	US-09-345-473E-40	Sequence 40, Appli
16	77.5	23.9	1601	2	US-09-862-027-40	Sequence 40, Appli
17	76.5	23.6	306	2	US-09-758-759-115	Sequence 115, App
18	76.5	23.6	395	2	US-09-247-155-113	Sequence 113, App
19	76.5	23.6	395	2	US-09-513-999C-14	Sequence 14, Appli
20	76.5	23.6	395	2	US-09-471-276-14	Sequence 14, Appli
21	76.5	23.6	395	2	US-09-903-190-113	Sequence 113, App
22	75.5	23.3	351	2	US-09-870-089B-2	Sequence 2, Appli
23	75.5	23.3	362	2	US-09-949-016-10923	Sequence 10923, A
24	75.5	23.3	501	2	US-09-949-016-11281	Sequence 11281, A
25	75.5	23.3	931	2	US-09-949-016-9850	Sequence 9850, Ap
26	74.5	23.0	338	1	US-08-218-686-2	Sequence 2, Appli
27	74.5	23.0	338	2	US-08-460-242-2	Sequence 2, Appli
28	74.5	23.0	452	2	US-09-949-016-7289	Sequence 7289, Ap
29	74	22.8	616	2	US-09-873-404-4	Sequence 4, Appli
30	74	22.8	616	2	US-10-243-735-4	Sequence 4, Appli
31	74	22.8	616	2	US-10-730-010-4	Sequence 4, Appli
32	73	22.5	551	2	US-08-796-899-29	Sequence 29, Appli
33	73	22.5	1637	2	US-09-718-692-2	Sequence 2, Appli
34	73	22.5	1637	2	US-09-718-852-2	Sequence 2, Appli
35	73	22.5	1637	2	US-09-718-815-2	Sequence 2, Appli
36	72.5	22.4	371	2	US-09-148-545-259	Sequence 259, App
37	72.5	22.4	371	2	US-09-621-011-259	Sequence 259, App
38	72	22.2	645	2	US-09-949-016-11022	Sequence 11022, A
39	72	22.2	650	2	US-09-487-558B-430	Sequence 430, App
40	72	22.2	700	2	US-09-831-642-34	Sequence 34, Appli
41	71	21.9	325	2	US-09-267-031-14	Sequence 14, Appli
42	71	21.9	802	2	US-09-823-240A-2	Sequence 2, Appli
43	70.5	21.8	118	2	US-09-134-001C-2856	Sequence 2856, Ap
44	70.5	21.8	182	2	US-09-640-211A-800	Sequence 800, App
45	70.5	21.8	307	2	US-09-267-031-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-533-029-104
; Sequence 104, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc

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start

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:33:51 ; Search time 18.56 Seconds
 (without alignments)
 331.782 Million cell updates/sec

Title: US-10-663-450-5_COPY_84_147

Perfect score: 323

Sequence: 1 EKKPVKKRKSWGQVLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	175	54.2	238	2	S78571	transcription fact
2	106	32.8	168	2	T50922	bZIP protein HY5 [
3	91	28.2	322	2	T08592	TGACG-motif-bindin
4	91	28.2	326	2	T08591	TGACG-motif bindin
5	90.5	28.0	688	2	T32750	hypothetical prote
6	88	27.2	322	2	T12093	TGACG-motif bindin
7	87.5	27.1	176	2	B90087	hypothetical prote
8	87	26.9	600	2	T00759	hypothetical prote

9	86	26.6	360	2	T03373	probable G-box bin
10	81	25.1	445	2	T50972	probable zuotin [i
11	80.5	24.9	486	2	JC4028	activating transcr
12	79.5	24.6	2052	2	T18519	myosin X - bovine
13	79	24.5	381	2	S26812	transcription fact
14	79	24.5	672	2	T21469	hypothetical prote
15	78.5	24.3	232	2	S42392	G-box-binding prot
16	78.5	24.3	242	2	S05453	transcription fact
17	78	24.1	424	2	T10985	regulator protein
18	77.5	24.0	246	2	T12585	Dc3 promoter-bindi
19	77.5	24.0	483	2	S12741	transcription fact
20	77.5	24.0	505	1	S05380	transcription fact
21	77	23.8	1089	2	T36663	protein kinase, tr
22	76.5	23.7	144	2	T14796	hypothetical prote
23	76.5	23.7	313	2	A34785	DNA-binding protei
24	76.5	23.7	351	2	A45377	transcription fact
25	76.5	23.7	358	2	C42026	cyclic AMP respons
26	76.5	23.7	389	1	A39429	cAMP response elem
27	76.5	23.7	448	2	A42026	cAMP response elem
28	76.5	23.7	456	2	B42026	cyclic AMP respons
29	76	23.5	502	2	T20130	hypothetical prote
30	76	23.5	521	2	S06218	colicin E1 - Shige
31	76	23.5	838	2	T20125	hypothetical prote
32	75.5	23.4	315	2	S20883	G-box-binding fact
33	75.5	23.4	315	2	G85433	G-box-binding fact
34	75.5	23.4	605	2	T02350	hypothetical prote
35	75	23.2	267	2	JC4857	hepatocarcinogenes
36	75	23.2	267	2	S51307	G-box binding fact
37	75	23.2	433	2	JC1230	DNA-binding protei
38	75	23.2	761	2	T00940	hypothetical prote
39	75	23.2	2062	2	A59297	myosin X - mouse
40	74.5	23.1	313	2	S66312	G-box binding fact
41	74.5	23.1	349	2	A41349	histone-specific t
42	74.5	23.1	349	2	S77570	transcription fact
43	74.5	23.1	452	2	H96710	hypothetical prote
44	74	22.9	331	2	T26807	hypothetical prote
45	74	22.9	333	2	T26808	hypothetical prote

ALIGNMENTS

RESULT 1

S78571

transcription factor HAC1 - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein YFL031w

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: S78571; S56223; S53578

R;Murakami, Y.

submitted to the Protein Sequence Database, January 1998

A;Reference number: S78570

A;Accession: S78571

A;Molecule type: DNA

A;Residues: 1-238

A;Cross-references: UNIPROT:P41546; UNIPARC:UPI0000157F61; EMBL:D50617; MIPS:YFL031w

A;Note: this is a revision to the sequence from reference S56186

R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasa submitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces*

A;Reference number: S56186

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-5_copy_84_147.rapbn.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:44:20 ; Search time 8.64 Seconds
(without alignments)
169.226 Million cell updates/sec

Title: US-10-663-450-5_COPY_84_147
Perfect score: 323
Sequence: 1 EKKPVKKRKSWGQVLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%
	Query

No.	Score	Match Length	DB	ID	Description
1	269	83.3	425	6 US-10-449-902-40262	Sequence 40262, A
2	103.5	32.0	134	6 US-10-953-349-13422	Sequence 13422, A
3	103.5	32.0	134	6 US-10-953-349-22329	Sequence 22329, A
4	103.5	32.0	191	6 US-10-953-349-13421	Sequence 13421, A
5	103.5	32.0	191	6 US-10-953-349-22328	Sequence 22328, A
6	94	29.1	646	6 US-10-449-902-51369	Sequence 51369, A
7	91	28.2	199	6 US-10-953-349-12209	Sequence 12209, A
8	91	28.2	201	6 US-10-953-349-20562	Sequence 20562, A
9	91	28.2	318	6 US-10-953-349-12208	Sequence 12208, A
10	91	28.2	320	6 US-10-953-349-20561	Sequence 20561, A
11	91	28.2	324	6 US-10-953-349-12207	Sequence 12207, A
12	91	28.2	326	6 US-10-953-349-20560	Sequence 20560, A
13	88	27.2	296	6 US-10-953-349-24027	Sequence 24027, A
14	88	27.2	362	6 US-10-953-349-24026	Sequence 24026, A
15	88	27.2	382	6 US-10-953-349-24025	Sequence 24025, A
16	82.5	25.5	611	7 US-11-321-421-81	Sequence 81, Appl
17	81	25.1	335	6 US-10-449-902-34705	Sequence 34705, A
18	80.5	24.9	293	6 US-10-953-349-23767	Sequence 23767, A
19	80.5	24.9	318	6 US-10-953-349-23766	Sequence 23766, A
20	80.5	24.9	323	6 US-10-953-349-23765	Sequence 23765, A
21	78	24.1	142	6 US-10-449-902-31867	Sequence 31867, A
22	77	23.8	380	6 US-10-449-902-43338	Sequence 43338, A
23	75.5	23.4	281	6 US-10-971-483-2	Sequence 2, Appli
24	75	23.2	332	6 US-10-953-349-23520	Sequence 23520, A
25	75	23.2	553	6 US-10-449-902-47325	Sequence 47325, A
26	74.5	23.1	237	6 US-10-953-349-34004	Sequence 34004, A
27	73.5	22.8	115	6 US-10-449-902-29417	Sequence 29417, A
28	73	22.6	167	6 US-10-449-902-40094	Sequence 40094, A
29	73	22.6	457	6 US-10-449-902-53115	Sequence 53115, A
30	73	22.6	523	6 US-10-449-902-56056	Sequence 56056, A
31	72	22.3	188	6 US-10-449-902-39656	Sequence 39656, A
32	71	22.0	393	6 US-10-449-902-41469	Sequence 41469, A
33	70.5	21.8	282	6 US-10-511-937-2600	Sequence 2600, Ap
34	70.5	21.8	467	6 US-10-449-902-38097	Sequence 38097, A
35	70.5	21.8	539	6 US-10-449-902-54234	Sequence 54234, A
36	70.5	21.8	784	6 US-10-449-902-41427	Sequence 41427, A
37	70	21.7	279	6 US-10-953-349-25745	Sequence 25745, A
38	70	21.7	400	6 US-10-449-902-39710	Sequence 39710, A
39	69.5	21.5	282	6 US-10-953-349-37838	Sequence 37838, A
40	69.5	21.5	308	6 US-10-953-349-37837	Sequence 37837, A
41	69.5	21.5	315	6 US-10-953-349-37836	Sequence 37836, A
42	69.5	21.5	330	6 US-10-449-902-53842	Sequence 53842, A
43	69.5	21.5	888	6 US-10-449-902-47557	Sequence 47557, A
44	69	21.4	156	6 US-10-953-349-25746	Sequence 25746, A
45	69	21.4	304	6 US-10-449-902-38130	Sequence 38130, A

ALIGNMENTS

RESULT 1

US-10-449-902-40262

; Sequence 40262, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-5_copy_84_147.rapbm.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:42:39 ; Search time 100.8 Seconds
(without alignments)
294.105 Million cell updates/sec

Title: US-10-663-450-5_COPY_84_147
Perfect score: 323
Sequence: 1 EKKPVKKRKSWGQVLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	323	100.0	451	3	US-09-816-277-2	Sequence 2, Appli
2	323	100.0	451	3	US-09-816-277-5	Sequence 5, Appli
3	323	100.0	451	4	US-10-663-450-2	Sequence 2, Appli
4	323	100.0	451	4	US-10-663-450-5	Sequence 5, Appli
5	307	95.0	409	3	US-09-533-029-104	Sequence 104, App
6	307	95.0	409	4	US-10-295-403-158	Sequence 158, App
7	307	95.0	409	4	US-10-412-699B-684	Sequence 684, App
8	292	90.4	342	3	US-09-816-277-19	Sequence 19, Appli
9	292	90.4	342	4	US-10-663-450-19	Sequence 19, Appli
10	292	90.4	386	3	US-09-816-277-16	Sequence 16, Appli
11	292	90.4	386	4	US-10-663-450-16	Sequence 16, Appli
12	288	89.2	349	3	US-09-816-277-4	Sequence 4, Appli
13	288	89.2	349	3	US-09-816-277-6	Sequence 6, Appli
14	288	89.2	349	4	US-10-663-450-4	Sequence 4, Appli
15	288	89.2	349	4	US-10-663-450-6	Sequence 6, Appli
16	268	83.0	174	4	US-10-767-701-61238	Sequence 61238, A
17	175	54.2	68	3	US-09-816-277-60	Sequence 60, Appli
18	175	54.2	68	4	US-10-663-450-60	Sequence 60, Appli
19	175	54.2	200	4	US-10-369-493-21867	Sequence 21867, A
20	108	33.4	147	4	US-10-425-115-187302	Sequence 187302,
21	108	33.4	192	3	US-09-772-656-2	Sequence 2, Appli
22	108	33.4	192	3	US-09-772-656-6	Sequence 6, Appli
23	108	33.4	192	3	US-09-772-656-10	Sequence 10, Appli
24	108	33.4	192	4	US-10-396-199A-2	Sequence 2, Appli
25	108	33.4	192	4	US-10-396-199A-6	Sequence 6, Appli
26	108	33.4	192	4	US-10-396-199A-10	Sequence 10, Appli
27	107	33.1	203	4	US-10-437-963-151695	Sequence 151695,
28	107	33.1	203	5	US-10-732-923-13694	Sequence 13694, A
29	107	33.1	203	5	US-10-732-923-13695	Sequence 13695, A
30	106	32.8	168	3	US-09-934-455-102	Sequence 102, App
31	106	32.8	168	4	US-10-225-066A-206	Sequence 206, App
32	106	32.8	168	4	US-10-374-780A-2356	Sequence 2356, Ap
33	106	32.8	168	5	US-10-732-923-13692	Sequence 13692, A
34	106	32.8	168	5	US-10-225-066A-206	Sequence 206, App
35	103.5	32.0	191	4	US-10-424-599-177263	Sequence 177263,
36	103	31.9	170	4	US-10-310-154-565	Sequence 565, App
37	102	31.6	109	5	US-10-732-923-13697	Sequence 13697, A
38	102	31.6	196	4	US-10-425-115-197786	Sequence 197786,
39	101	31.3	665	4	US-10-425-115-190929	Sequence 190929,
40	101	31.3	672	4	US-10-425-114-58469	Sequence 58469, A
41	99	30.7	143	5	US-10-856-499-1930	Sequence 1930, Ap
42	98	30.3	176	4	US-10-437-963-164243	Sequence 164243,
43	97	30.0	181	5	US-10-732-923-450	Sequence 450, App
44	95	29.4	217	4	US-10-425-115-197783	Sequence 197783,
45	94	29.1	114	4	US-10-425-115-246430	Sequence 246430,

ALIGNMENTS

RESULT 1

US-09-816-277-2

; Sequence 2, Application US/09816277
; Publication No. US20010034045A1
; GENERAL INFORMATION:
; APPLICANT: Penttila, Merja E.
; APPLICANT: Ward, Michael
; APPLICANT: Wang, Huaming
; APPLICANT: Valkonen, Mari J.
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Increased Production of Secreted